

Schreiber, David

88846

From: Steadman, David (AU1652)
Sent: Wednesday, March 05, 2003 3:39 PM
To: Schreiber, David
Subject: 09/526,193 sequence search request

NAME: David Steadman
AU: 1652
Date: 03/05/03
Office: 10D-04
Mailbox: 10D-01

Mr. Schreiber, please search the following sequences in commercial and interference databases:

- 1) Standard search of amino acids 1-60 of SEQ ID NO:1 against **amino** acid databases.
- 2) Standard search of SEQ ID NO:1 against **nucleic** acid databases.
- 3) Standard search of SEQ ID NO:1 against **amino** acid databases.

Please save results to diskette.

Thank you very much.

David J. Steadman
Art Unit 1652
Crystal Mall 1 Room 10D-04
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Phosphorylation site prediction for sequence DJS

Sequence identifier: **DJS**

Number of residues: **2201**

Full sequence:

MPSAGTLPWVQGIICNANNPCFRYPTPGEAPGVVGNFNKSIVARLFSDARRLLLYSQKDTSMKDMRKVLRRTLQQIKK
 NLKLQDFLVDNETFSGFLYHNLSLPKSTVDKMLRADVILHKVFLQGYQLHLTSLCNGSKSEEMIQLGDQEVSEL CGL
 KLAAAERVLRSNMDILKPIRLTNSTSPFPKELAEATKTLHSLGTLAQELFSMRSWSDMRQEV MFLTNVNSSSSS
 YQAVSRIVCGHPEGGLKIKSLNWEYEDNNYKALFGGNGTEEDAETFYDNSTTPYCNDLMKNLESSPLSRIIWKALKP
 GKILYTPDTPATRQVMAEVNKTFOELAVFHDLEGMWEELSPKIWTFMENSQEMDLVRMLLDSRDNDHFWEQQLDGLD
 QDIVAFLAKHPEDVQSSNGSVYTWEAFNETNQAI RTISRMECVNLNKLEPIATEVWLINKSMELLDERKFWAGIV
 ITPGSIELPHHVYKIRMDIDNVERTNKIKDGYWDPGPRADPFEDMRYVWGGFAYLQDVVEQAIIRVLTGT EKKTG
 QMPYP CYVDDIFLRVMSRSMPLFMTLAWIYSVAVIKIGIVYEKEARLKETMRIMGLDNSILWFSWFISSLIPLLVSA
 VVILKLGNNLPYSDPSVVFVFLSVFAVVTILQCFLISTLFSRANLAAACGGIIYFTLYLPYVLCVAWQDYVGFTLKI
 LLSPVAFGFGCEYFALFEEQGIGVQWDNLFESPVEEDGFNLTTSVSMMLFDTFLYGVM TWYIEAVFPGQYGI PRPWY
 TKSYWFGESDEKSHPGSNQKRIS EICMEEETHLKLGVSIQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGA
 TTMSILTGLFPPTSGTAYILGKDIRSEMSTIRQNLGVCPOHNVLFDMLTVEEHIWFYARL KGLSEKHVKAEME QMAL
 LPSSKLKSKTSQLSGGMQRKLSVALAFVGGSKVILDEPTAGVDPYSRRGIWELLLKYRQRTIILSTHMD EADV
 IAIISHGKLCCVGSSFLKNQLGTGYLTLVKKDVESSLSSCRNSSSTVSYLK KEDSVSQSSSDAGLGS DHESDTLT
 SAISNLIRKHVSEARLVEDIGHELT YVLPYEAKEGAFVELFHEIDDRLSDLGISSYGISETTLEE IFLKVAEESGV
 TSDGTL PARRNRRAFGDKQSC LRPFTEDDAADPNDSIDPESRETDL LSGMDGKGSYQVKGWKL TQQQFVALLWKRL
 RRSRKGFFAQIVLP AVFVCI ALVFS L IVPFPGKYPSLELQPW MYNEQYTFVSNDA PEDTGTLELLNALT KDPGFGTR
 GNPIPDTPCQAGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRKQNTADIL
 TGRNISDYL VKTYVQIIAKSLKNKIWN EFRYGGFSLGVSN TQALPPSQEVNDATKQMKKHLKLAKDSSADRFLNSL
 MTGLDTRNNVKVWFNNKGWHAISSFLNVINNA ILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVAPMTTSVDVLV
 VIFAMSFVPASFVFLIQERVSKAKHLQFISGVKPV IYWLSNFVWDMCNYVVPATLVIIIFICFQQKSYVSSSTNLPV
 LLLLYGWSITPLMYPASFVFKIPSTAYVVLTSVNLFIGINGSVATFVLELFTDNKLNNINDILKSVFLIFPHFCLGR
 DMVKNQAMADALERFGENRFVSPLSWDLVGRNLFAMAVEGVVFFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRR
 RILDGGGQNDILEIKELTKIYRRKRKPAVDRI CVGIPPGECFGLLG VNGAGKSSTFKMLTGD TTVTRGD AFLNRNSI
 IHEVHQNMGYCQPFDAITELLTGREHVEFFALLRGVPEKEVGKVG EWAI RKLGLVKYGEKYAGNYSGGNKRKLSTAM
 GGPPVVFLDEPTTGMDPKARRFLWNCALSVVKEGRSVLTS HSMEECEALCTRMAIMVNGRFRCLG SVQHLKNRFGD
 IVVRIAGSNPDLKPVDQDFGLAFPGSVPEKHRNMLQYQLPSSLSLARIFSILSQSKRLHI EDYSVSQTTLDQVF
 AKDQSDDDHLKDL SLHKNQTVVDVAVLTSFLQDEKVKESYV

The prediction is based on the consensus sequence motifs. For the list of the used motifs see [here](#).

The consensus sequences for 10 different protein kinases are scanned for potential phosphorylation sites.

Potential phosphorylation sites for protein kinase CaMII:

- T-26 RYPTPGE
- S-47 RLFSDAR
- S-219 RSWSDMR
- S-439 RTISRFM
- T-549 RVLTGTE
- S-577 RVMSRSM
- S-982 RKLSVAL
- S-1086 RNSSSTV

- T-1226 RPFTEDD
- S-1446 RNISDYL
- T-1522 RFMTGLD
- S-1782 RFVSPLS
- S-1994 RKLSTAM
- S-2132 RIFSILS

Potential phosphorylation sites for protein kinase CKI (N-terminal S/T must be prephosphorylated):

- T-6 SAGTLPW
- T-60 SQKDTSMK
- S-107 SLPKSTVD
- T-186 TLNSTSPF
- S-191 SPFPSKEL
- S-204 TLLHSLGT
- S-217 SMRSWSD
- S-233 TNVNSSSS
- T-238 SSSSTQIY
- S-308 SSPLSR II
- T-329 TPDTPAT
- S-420 SSNGSVYT
- T-482 TGITPGS
- T-555 TEKKTGVY
- S-628 SWFISSLI
- S-656 SDPSVVF
- S-681 STLFSRAN
- S-723 SLLSPVA
- S-766 TTSVSMML
- S-814 SDEKSHPG
- S-884 TTTMSILT

- T-896 TSGTAYI
- T-910 SEMSTIRQ
- S-968 SKLKSKTS
- S-974 TSQLSGGM
- S-1027 TIILSTHH
- S-1081 SSLSSCRN
- T-1088 SSSTVSY
- S-1101 SVSQSSSD
- S-1113 SDHESDTL
- S-1121 TIDVSAIS
- S-1180 SYGISETT
- T-1205 TSDGTLPA
- T-1245 SRETDLL
- S-1332 TFVSNDA
- S-1480 SLGVSNTQ
- T-1526 TGLDTRNN
- S-1672 SYVSSTNL
- T-1725 SVATFVL
- S-1785 SPLSWDL
- T-1904 TGDTTVTR
- S-1919 SILSNIH
- T-1942 TELLTGRE
- T-2040 SVVLTSHS
- S-2126 SSLSSLAR
- S-2135 SILSQSK
- T-2151 SVSQTTLD

Potential phosphorylation sites for protein kinase CKII:

- T-26 RYPTPGE

- S-56 LLYSQKD
- S-61 KDTSMKD
- S-107 LPKSTVD
- S-138 CNGSKSE
- S-171 VLRSNMD
- S-217 SMRSWSD
- T-279 GNGTEED
- T-285 DAETFYD
- T-342 VNKTFQE
- T-365 KIWTFME
- T-399 LDWTAQD
- T-423 SVYTWRE
- T-549 RVLGTGE
- S-752 LFESPVE
- T-929 DMLTVEE
- S-1101 VSQSSSD
- S-1109 GLGSDHE
- T-1182 ISETTLE
- S-1195 AEESGVD
- T-1226 RPFTEDD
- S-1236 PNDSID
- S-1249 DLLSGMD
- T-1384 VPQTIMD
- S-1508 AKDSSAD
- T-1522 RFMTGLD
- T-1591 PMTTSVD
- T-1906 TTVTRGD
- T-1942 ELLTGRE

- T-2013 EPTTGMD
- S-2043 TSHSMEE
- S-2088 IAGSNPD
- T-2151 VSQTTLD
- S-2165 KDQSDDD
- T-2180 KNQTVVD

Potential phosphorylation sites for protein kinase GSK3 (C-terminal +4 S must be prephosphorylated):

- S-103 HNLSLPKS
- S-187 NSTSPFPS
- T-200 ATKTLHLS
- T-229 MFLTINVNS
- S-233 NVNSSSSS
- S-304 NLESSPLS
- S-416 DVQSSNGS
- S-624 LWFSWFIS
- S-677 FLISTLFS
- T-762 FNLTTSVS
- S-810 GEESDEKS
- S-814 DEKSHPGS
- T-880 AGKTTTMS
- S-964 LPSSKLKS
- T-970 KSKTSQLS
- T-1023 QGRTIILS
- S-1077 DVESSLSS
- S-1081 SLSSCRNS
- S-1086 RNSSSTVS
- S-1097 KEDSVSQS
- S-1109 GLGSDHES